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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/923,444

DATE: 11/14/2001
 TIME: 12:13:13

Input Set : N:\Crf3\RULE60\09923444.txt
 Output Set: N:\CRF3\11142001\I923444.raw

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 TECH CENTER 1600/2900

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: LI, YI

7 FLEISCHMANN, ROBERT

9 (ii) TITLE OF INVENTION: NEUROTRANSMITTER TRANSPORTER

11 (iii) NUMBER OF SEQUENCES: 6

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Human Genome Sciences, Inc.

15 (B) STREET: 9410 Key West Avenue

16 (C) CITY: Rockville

17 (D) STATE: MD

18 (E) COUNTRY: US

19 (F) ZIP: 20850

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/923,444

C--> 29 (B) FILING DATE: 08-Aug-2001

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 09/062,815

34 (B) FILING DATE: 1998-04-20

35 (viii) ATTORNEY/AGENT INFORMATION:

36 (A) NAME: Michele M. Wales

37 (B) REGISTRATION NUMBER: 43,975

38 (C) REFERENCE/DOCKET NUMBER: PF116

40 (ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: (301) 309-8504

42 (B) TELEFAX: (301) 309-8439

45 (2) INFORMATION FOR SEQ ID NO: 1:

47 (i) SEQUENCE CHARACTERISTICS:

48 (A) LENGTH: 2485 base pairs

49 (B) TYPE: nucleic acid

50 (C) STRANDEDNESS: single

51 (D) TOPOLOGY: linear

53 (ii) MOLECULE TYPE: DNA (genomic)

56 (ix) FEATURE:

57 (A) NAME/KEY: CDS

58 (B) LOCATION: 266..2446

61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

63	CGGAGGCAGG	GAGTGAGGAG	CGAGCGGAGT	CGCGTGCGCC	GGCGCGAGCT	CCGGGTCGCC	60
65	CCAGCCCCAG	CCGGGGGCCT	GTGGCGGGGG	AGGAGCTGTG	CGTCCGCGAC	CCGTCCGGAT	120
67	CGCAGCTGCT	CGGCCGGAGT	GCACGGGCCG	AGTCTGCGCG	ACTACCCACG	CGTGACAGGT	180
69	CCCTGAATGA	GAAGGAGCTG	ACAGCAGCTG	AATTCATCT	TCTCTGTGTG	CTGGGGAGCA	240

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71	GGGCTACACG	CCCCAGGTGG	CATCA	ATG	CCG	AAG	AAC	AGC	AAA	GTG	ACC	CAG	292
72				Met	Pro	Lys	Asn	Ser	Lys	Val	Thr	Gln	
73				1				5					
75	CGT	GAG	CAC	AGC	AGT	GAG	CAT	GTC	ACT	GAG	TCC	GTG	340
76	Arg	Glu	His	Ser	Ser	Glu	His	Val	Thr	Glu	Ser	Val	
77	10				15				20			25	
79	GCC	CTC	GAG	GAG	CCT	GTG	GAC	TAT	AAG	CAG	AGT	GTA	388
80	Ala	Leu	Glu	Glu	Pro	Val	Asp	Tyr	Lys	Gln	Ser	Val	
81				30				35				40	
83	GGT	GAG	GCA	GGC	GGC	AAG	CAG	AAG	GCG	GTG	GAG	GAG	436
84	Gly	Glu	Ala	Gly	Gly	Lys	Gln	Lys	Ala	Val	Glu	Glu	
85			45			50					55		
87	GAG	GAC	CGG	CCG	GCC	TGG	AAC	AGT	AAG	CTG	CAG	TAC	484
88	Glu	Asp	Arg	Pro	Ala	Trp	Asn	Ser	Lys	Leu	Gln	Tyr	
89		60				65					70		
91	ATT	GGC	TTC	TCT	GTG	GGC	CTC	GGC	AAC	ATC	TGG	AGG	532
92	Ile	Gly	Phe	Ser	Val	Gly	Leu	Gly	Asn	Ile	Trp	Arg	
93		75				80					85		
95	TGC	CAG	AAA	AAT	GGA	GGA	GCT	TAC	CTG	GTG	CCC	TAC	580
96	Cys	Gln	Lys	Asn	Gly	Gly	Gly	Ala	Tyr	Leu	Val	Pro	
97	90				95				100			105	
99	CTG	ATC	ATC	ATC	GGG	ATC	CCC	CTC	TTC	TTC	CTG	GAG	628
100	Leu	Ile	Ile	Ile	Gly	Ile	Pro	Leu	Phe	Phe	Leu	Glu	
101				110					115			120	
103	CAG	AGG	ATC	CGC	CGC	GGA	AGC	ATC	GGT	GTG	TGG	CAC	676
104	Gln	Arg	Ile	Arg	Arg	Gly	Ser	Ile	Gly	Val	Trp	His	
105			125					130				135	
107	CGC	CTG	GGG	GGG	ATC	GGC	TTC	TCC	AGC	TGC	ATA	GTC	724
108	Arg	Leu	Gly	Gly	Ile	Gly	Phe	Ser	Ser	Cys	Ile	Val	
109			140				145					150	
111	GGG	CTG	TAT	TAT	AAT	GTG	ATC	ATC	GGG	TGG	AGC	ATC	772
112	Gly	Leu	Tyr	Tyr	Asn	Val	Ile	Ile	Gly	Trp	Ser	Ile	
113		155				160					165		
115	AAG	TCC	TTC	CAG	TAC	CCG	CTG	CCC	TGG	AGT	GAA	TGT	820
116	Lys	Ser	Phe	Gln	Tyr	Pro	Leu	Pro	Trp	Ser	Glu	Cys	
117	170				175					180		185	
119	AAT	GGG	AGC	GTC	GCA	GTG	GTG	GAG	GCA	GAG	TGT	GAA	868
120	Asn	Gly	Ser	Val	Ala	Val	Val	Glu	Ala	Glu	Cys	Glu	
121				190					195			200	
123	ACT	ACC	TAC	TTC	TGG	TAC	CGA	GAG	GCT	TTG	GAC	ATC	916
124	Thr	Thr	Tyr	Phe	Trp	Tyr	Arg	Glu	Ala	Leu	Asp	Ile	
125			205					210				215	
127	TCG	GAG	AGT	GGG	GGC	CTC	AAC	TGG	AAG	ATG	ACC	CTG	964
128	Ser	Glu	Ser	Gly	Gly	Leu	Asn	Trp	Lys	Met	Thr	Leu	
129			220				225					230	
131	GTC	TGG	AGC	ATC	GGG	GGG	ATG	GCT	GTC	GGT	AAG	GGC	1012
132	Val	Trp	Ser	Ile	Gly	Gly	Met	Ala	Val	Gly	Lys	Gly	
133		235				240					245		
135	GGG	AAG	GTG	ATG	TAT	TTC	AGC	TCC	CTC	TTC	CCC	TAC	1060

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136	Gly	Lys	Val	Met	Tyr	Phe	Ser	Ser	Leu	Phe	Pro	Tyr	Val	Val	Leu	Ala	
137	250					255					260					265	
139	TGC	TTC	CTG	GTC	CGG	GGG	TTG	TTG	TTG	CGA	GGG	GCA	GTT	GAT	GGC	ATC	1108
140	Cys	Phe	Leu	Val	Arg	Gly	Leu	Leu	Leu	Arg	Gly	Ala	Val	Asp	Gly	Ile	
141					270					275						280	
143	CTA	CAC	ATG	TTC	ACT	CCC	AAG	CTG	GTC	AAG	ATG	CTG	GAC	CCC	CAG	GTG	1156
144	Leu	His	Met	Phe	Thr	Pro	Lys	Leu	Val	Lys	Met	Leu	Asp	Pro	Gln	Val	
145					285					290						295	
147	TGG	CGG	GAG	GTA	GCT	ACC	CAG	GTC	TTC	TTT	GGC	TTG	GGT	CTG	GGC	TTT	1204
148	Trp	Arg	Glu	Val	Ala	Thr	Gln	Val	Phe	Phe	Gly	Leu	Gly	Leu	Gly	Phe	
149			300						305					310			
151	GGT	GGT	GTC	ATT	GTC	TTC	TCC	AGT	TAC	AAT	AAG	CAG	GAC	AAC	AAC	TGC	1252
152	Gly	Gly	Val	Ile	Val	Phe	Ser	Ser	Tyr	Asn	Lys	Gln	Asp	Asn	Asn	Cys	
153		315					320					325					
155	CAC	TTC	GAT	GGC	GCC	CTG	GTG	TCC	TTC	ATC	AAC	TTC	TTC	ACG	TCA	GTG	1300
156	His	Phe	Asp	Gly	Ala	Leu	Val	Ser	Phe	Ile	Asn	Phe	Phe	Thr	Ser	Val	
157	330					335					340					345	
159	TTG	GCC	ACC	CTC	GTG	GTG	TTT	GTT	GTT	TTG	GGC	TTC	AAG	GCC	AAC	ATC	1348
160	Leu	Ala	Thr	Leu	Val	Val	Phe	Val	Val	Leu	Gly	Phe	Lys	Ala	Asn	Ile	
161					350					355						360	
163	ATG	AAT	GAG	AAG	TGT	GTG	GTC	GAG	AAT	GCT	GAG	AAA	ATC	CTA	GGG	TAC	1396
164	Met	Asn	Glu	Lys	Cys	Val	Val	Glu	Asn	Ala	Glu	Lys	Ile	Leu	Gly	Tyr	
165			365					370					375				
167	CTT	AAC	ACC	AAC	GTC	CTG	AGC	CGG	GAC	CTC	ATC	CCA	CCC	CAC	GTC	AAC	1444
168	Leu	Asn	Thr	Asn	Val	Leu	Ser	Arg	Asp	Leu	Ile	Pro	Pro	His	Val	Asn	
169			380					385					390				
171	TTC	TCC	CAC	CTG	ACC	ACA	AAG	GAC	TAC	ATG	GAG	ATG	GAC	AAT	GTC	ATC	1492
172	Phe	Ser	His	Leu	Thr	Thr	Lys	Asp	Tyr	Met	Glu	Met	Asp	Asn	Val	Ile	
173		395					400					405					
175	ATG	ACC	GTG	AAG	GAG	GAC	CAG	TTC	TCA	GCC	CTG	GGC	CTT	GAC	CCC	TGC	1540
176	Met	Thr	Val	Lys	Glu	Asp	Gln	Phe	Ser	Ala	Leu	Gly	Leu	Asp	Pro	Cys	
177	410					415				420						425	
179	CTT	CTG	GAG	GAC	GAG	CTG	GAC	AAG	TCC	GTG	CAG	GGC	ACA	GGC	CTG	GCC	1588
180	Leu	Leu	Glu	Asp	Glu	Leu	Asp	Lys	Ser	Val	Gln	Gly	Thr	Gly	Leu	Ala	
181				430					435							440	
183	TTC	ATC	GCC	TTC	ACT	GAG	GCC	ATG	ACG	CAC	TTC	CCC	ACC	TCC	CCG	TTC	1636
184	Phe	Ile	Ala	Phe	Thr	Glu	Ala	Met	Thr	His	Phe	Pro	Thr	Ser	Pro	Phe	
185			445					450					455				
187	TGG	TCC	GTC	ATG	TTC	TTC	TTG	ATG	CTT	ATC	AAC	CTG	GGC	CTG	GGC	AGC	1684
188	Trp	Ser	Val	Met	Phe	Phe	Leu	Met	Leu	Ile	Asn	Leu	Gly	Leu	Gly	Ser	
189			460					465					470				
191	ATG	ATC	GGG	ACC	ATG	GCA	GGC	ATC	ACC	ACG	CCC	ATC	ATC	GAC	ACC	TCC	1732
192	Met	Ile	Gly	Thr	Met	Ala	Gly	Ile	Thr	Thr	Pro	Ile	Ile	Asp	Thr	Ser	
193		475					480					485					
195	AAG	GTG	CCC	AAG	GAG	ATG	TTC	ACA	GTG	GGC	TGC	TGT	GTC	TTT	ACA	TTC	1780
196	Lys	Val	Pro	Lys	Glu	Met	Phe	Thr	Val	Gly	Cys	Cys	Val	Phe	Thr	Phe	
197	490					495				500						505	
199	CTC	GTG	GGA	CTG	TTG	TTC	GTC	CAG	CGC	TCC	GGA	AAC	TAC	TTT	GTC	ACC	1828
200	Leu	Val	Gly	Leu	Leu	Phe	Val	Gln	Arg	Ser	Gly	Asn	Tyr	Phe	Val	Thr	

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201          510          515          520
203 ATG TTC GAT GAC TAC TCA GCC ACG CTG CCA CTC ACT CTC ATC GTC ATC 1876
204 Met Phe Asp Asp Tyr Ser Ala Thr Leu Pro Leu Thr Leu Ile Val Ile
205          525          530          535
207 CTT GAG AAC ATC GCT GTG GCC TGG ATT TAT GGA CCC AAG AAG TTC ATG 1924
208 Leu Glu Asn Ile Ala Val Ala Trp Ile Tyr Gly Pro Lys Lys Phe Met
209          540          545          550
211 CAG GAG CTG ACG GAG ATG CTG GGC TTC CGC CCC TAC CGC TTC TAT TTC 1972
212 Gln Glu Leu Thr Glu Met Leu Gly Phe Arg Pro Tyr Arg Phe Tyr Phe
213          555          560          565
215 TAC ATG TGG AAG TTC GTG TCT CCA CTA TGC ATG GCT GTG CTC ACC ACA 2020
216 Tyr Met Trp Lys Phe Val Ser Pro Leu Cys Met Ala Val Leu Thr Thr
217 570          575          580
219 GCC AGC ATC ATC CAG CTG GGG GTC ACG CCC CCG GCC TAC AGC GCC TGG 2068
220 Ala Ser Ile Ile Gln Leu Gly Val Thr Pro Pro Ala Tyr Ser Ala Trp
221          590          595
223 ATC AAG GAG GAG GCT GCC GAG CGC TAC CTG TAT TTC CCC AAC TGG CCC 2116
224 Ile Lys Glu Glu Ala Ala Glu Arg Tyr Leu Tyr Phe Pro Asn Trp Pro
225          605          610          615
227 ATG GCA CTC CTG ATC ACC CTC ATC GTC GTG GCG ACG CTG CCC ATC CCT 2164
228 Met Ala Leu Leu Ile Thr Leu Ile Val Val Ala Thr Leu Pro Ile Pro
229          620          625          630
231 GTG GTG TTC GTC CTG CGG CAC TTC CAC CTG CTC TCT GAT GGC TCC AAC 2212
232 Val Val Phe Val Leu Arg His Phe His Leu Leu Ser Asp Gly Ser Asn
233          635          640          645
235 ACC CTC TCC GTG TCC TAC AAG AAG GCC CGC ATG ATG AAG GAC ATC TCC 2260
236 Thr Leu Ser Val Ser Tyr Lys Lys Ala Arg Met Met Lys Asp Ile Ser
237 650          655          660
239 AAC CTG GAG GAG AAC GAT GAG ACC CGC TTC ATC CTC AGC AAG GTG CCC 2308
240 Asn Leu Glu Glu Asn Asp Glu Thr Arg Phe Ile Leu Ser Lys Val Pro
241          670          675
243 AGT GAG GCA CCT TCC CCC ATG CCC ACT CAC CGT TCC TAT CTG GGG CCC 2356
244 Ser Glu Ala Pro Ser Pro Met Pro Thr His Arg Ser Tyr Leu Gly Pro
245          685          690          695
247 GGC AGC ACA TCA CCC CTG GAG ACC AGC TGG AAC CCC AAT GGA CCC TAT 2404
248 Gly Ser Thr Ser Pro Leu Glu Thr Ser Trp Asn Pro Asn Gly Pro Tyr
249          700          705          710
251 GGG CGC GGC TAC CTG CTG GCC AGC ACC CCT GAG TCT GAG CTG 2446
252 Gly Arg Gly Tyr Leu Leu Ala Ser Thr Pro Glu Ser Glu Leu
253          715          720          725
255 TGACCACTGC CCAAGCCCAT GCCCGCTCTC CCCCCACCG 2485
258 (2) INFORMATION FOR SEQ ID NO: 2:
260 (i) SEQUENCE CHARACTERISTICS:
261 (A) LENGTH: 727 amino acids
262 (B) TYPE: amino acid
263 (D) TOPOLOGY: linear
265 (ii) MOLECULE TYPE: protein
267 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
269 Met Pro Lys Asn Ser Lys Val Thr Gln Arg Glu His Ser Ser Glu His

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270      1              5              10              15
272 Val Thr Glu Ser Val Ala Asp Leu Leu Ala Leu Glu Glu Pro Val Asp
273              20              25              30
275 Tyr Lys Gln Ser Val Leu Asn Val Ala Gly Glu Ala Gly Gly Lys Gln
276              35              40              45
278 Lys Ala Val Glu Glu Glu Leu Asp Ala Glu Asp Arg Pro Ala Trp Asn
279              50              55              60
281 Ser Lys Leu Gln Tyr Ile Leu Ala Gln Ile Gly Phe Ser Val Gly Leu
282      65              70              75              80
284 Gly Asn Ile Trp Arg Phe Pro Tyr Leu Cys Gln Lys Asn Gly Gly Gly
285              85              90              95
287 Ala Tyr Leu Val Pro Tyr Leu Val Leu Leu Ile Ile Ile Gly Ile Pro
288              100              105              110
290 Leu Phe Phe Leu Glu Leu Ala Val Gly Gln Arg Ile Arg Arg Gly Ser
291              115              120              125
293 Ile Gly Val Trp His Tyr Ile Cys Pro Arg Leu Gly Gly Ile Gly Phe
294              130              135              140
296 Ser Ser Cys Ile Val Cys Leu Phe Val Gly Leu Tyr Tyr Asn Val Ile
297      145              150              155              160
299 Ile Gly Trp Ser Ile Phe Tyr Phe Phe Lys Ser Phe Gln Tyr Pro Leu
300              165              170              175
302 Pro Trp Ser Glu Cys Pro Val Val Arg Asn Gly Ser Val Ala Val Val
303              180              185              190
305 Glu Ala Glu Cys Glu Lys Ser Ser Ala Thr Thr Tyr Phe Trp Tyr Arg
306              195              200              205
308 Glu Ala Leu Asp Ile Ser Asp Ser Ile Ser Glu Ser Gly Gly Leu Asn
309              210              215              220
311 Trp Lys Met Thr Leu Cys Leu Leu Val Val Trp Ser Ile Gly Gly Met
312      225              230              235              240
314 Ala Val Gly Lys Gly Ile Gln Ser Ser Gly Lys Val Met Tyr Phe Ser
315              245              250              255
317 Ser Leu Phe Pro Tyr Val Val Leu Ala Cys Phe Leu Val Arg Gly Leu
318              260              265              270
320 Leu Leu Arg Gly Ala Val Asp Gly Ile Leu His Met Phe Thr Pro Lys
321              275              280              285
323 Leu Val Lys Met Leu Asp Pro Gln Val Trp Arg Glu Val Ala Thr Gln
324              290              295              300
326 Val Phe Phe Gly Leu Gly Leu Gly Phe Gly Gly Val Ile Val Phe Ser
327      305              310              315              320
329 Ser Tyr Asn Lys Gln Asp Asn Asn Cys His Phe Asp Gly Ala Leu Val
330              325              330              335
332 Ser Phe Ile Asn Phe Phe Thr Ser Val Leu Ala Thr Leu Val Val Phe
333              340              345              350
335 Val Val Leu Gly Phe Lys Ala Asn Ile Met Asn Glu Lys Cys Val Val
336              355              360              365
338 Glu Asn Ala Glu Lys Ile Leu Gly Tyr Leu Asn Thr Asn Val Leu Ser
339              370              375              380
341 Arg Asp Leu Ile Pro Pro His Val Asn Phe Ser His Leu Thr Thr Lys
342      385              390              395              400

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]